

Fig. 1

Signal peptide
MTRSPALLLLLLGALPSAEAAAR / GPPRMADKVVPRQVARLGRTVRLQCPVEGDPPPLTMWTKDGRTIHSGWS
 1 20 40 IgG1 domain

RFRVLPQGLKVKEVEAEDAGVYVCKATNGFGSLSVNYTLIIM / DDISPGKESPGPGSSGGQEDPASQQWAR
 102

PRFTQPSKMRRRVIARPVGSSVRLKCVASGHPRPDIMWMKDDQTLTHLEASEHRKKKWTLSLKNLKPEDSG
 161 IgG2 domain

KYTCRVSNKAGAINATYKVDVIQRTSRKPVLTGTHPVNTTVDFGGTTSFQCKVRSDVKPVIQWLKRVEYGS
 224 258

EGRHNSTIDVGGQKFVVLPTGDVWSRPDGSYLNKLLISRARQDDAGMYICLGANTMGVSFRSAFLTVLPDP
 341

KPPGPPMASSSSSTSLPWFPVVIGIPAGAVFILGTVLLWLCQTKKKPCAPASTLPVPGHRPPGTSRERSGDK
 374 394 Transmembrane domain

DLPSLAVGICEEHGSAMAPQHILASGSTAGPKLYPKLYTDVHTHTHTCTHTLSCGGQGSSTPACPLSVL
 529

NTANLQALCPEVGIWGPQQVGRIENNGGRVS

Underlined: Signal peptide, IgG1 domain, IgG2 domain, Transmembrane domain

Bold, Italics, underlined: Four putative glycosylation sites

Bold, underlined: putative SHP-2 binding site:

/...../ : Splice sites for FGFRγ

Fig. 2A

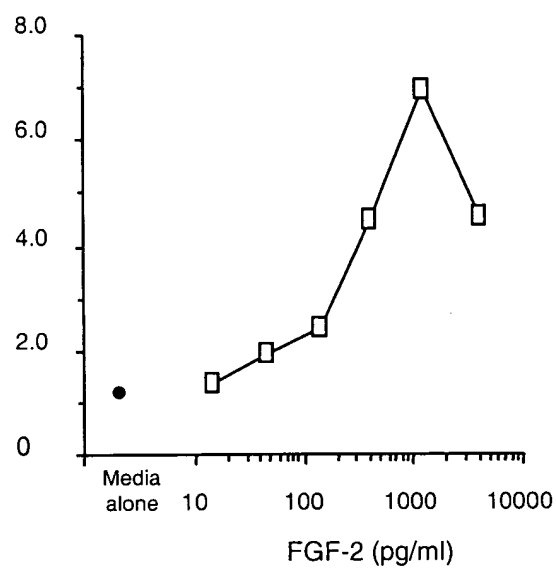


Fig. 2B

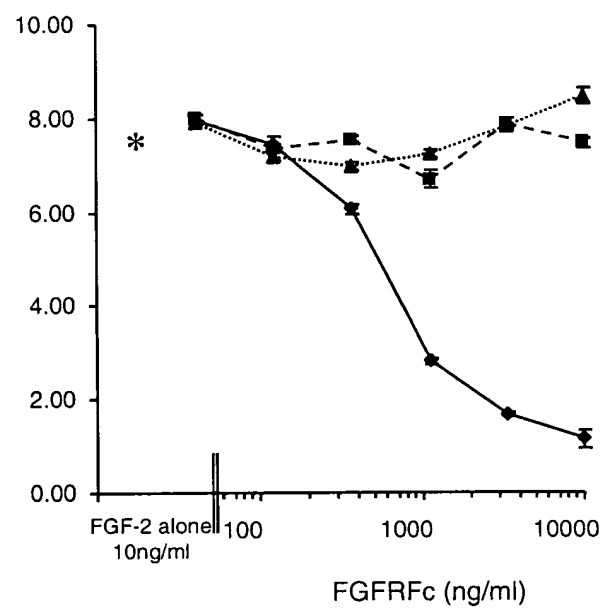


Figure 3 shows the effect of various concentrations of FGFR5 β , FGFR5 γ , FGFR2, and FGF-2 on MTS conversion. The x-axis represents the concentration in nM on a logarithmic scale, and the y-axis represents the MTS conversion (Mean OD \pm SD). The legend indicates that FGFR5 β is represented by open circles, FGFR5 γ by filled triangles, FGFR2 by open squares, FGF-2 by filled circles, and Media by a solid line. The data points are plotted with error bars representing standard deviation. The MTS conversion generally increases with increasing concentration for all factors, with FGFR5 β and FGFR5 γ showing the highest activity at higher concentrations.

Fig. 3

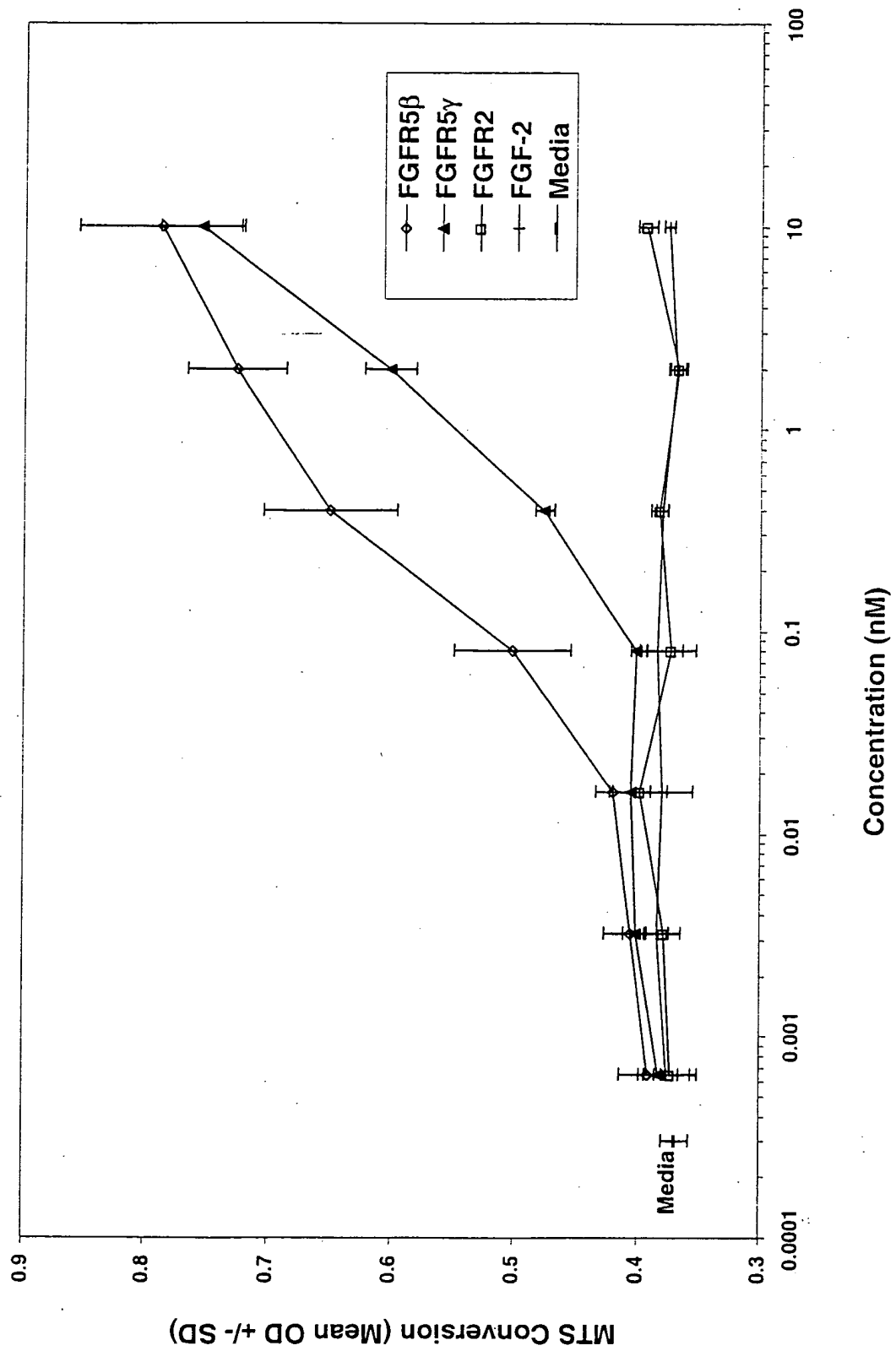


Fig. 4

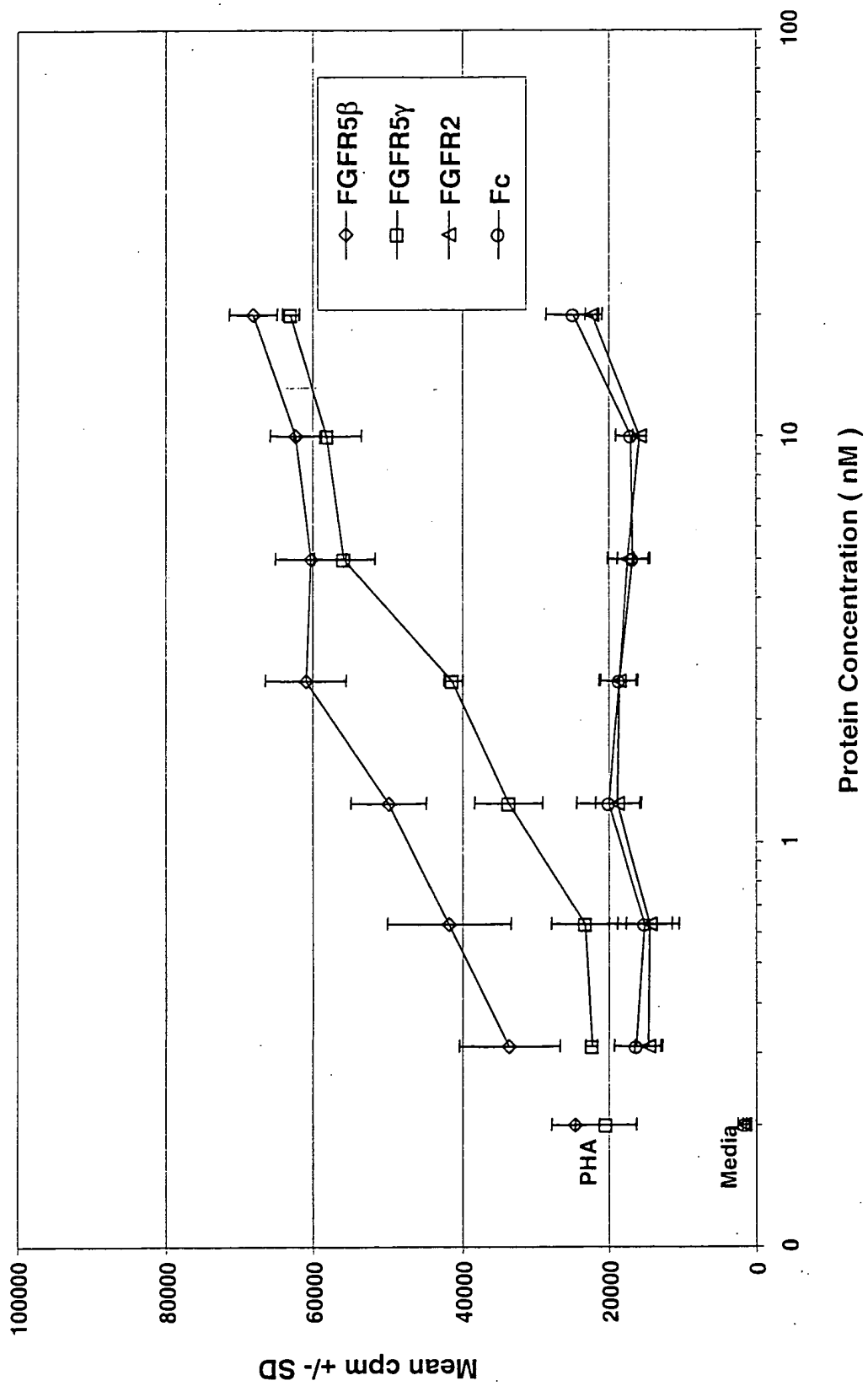


Fig. 5

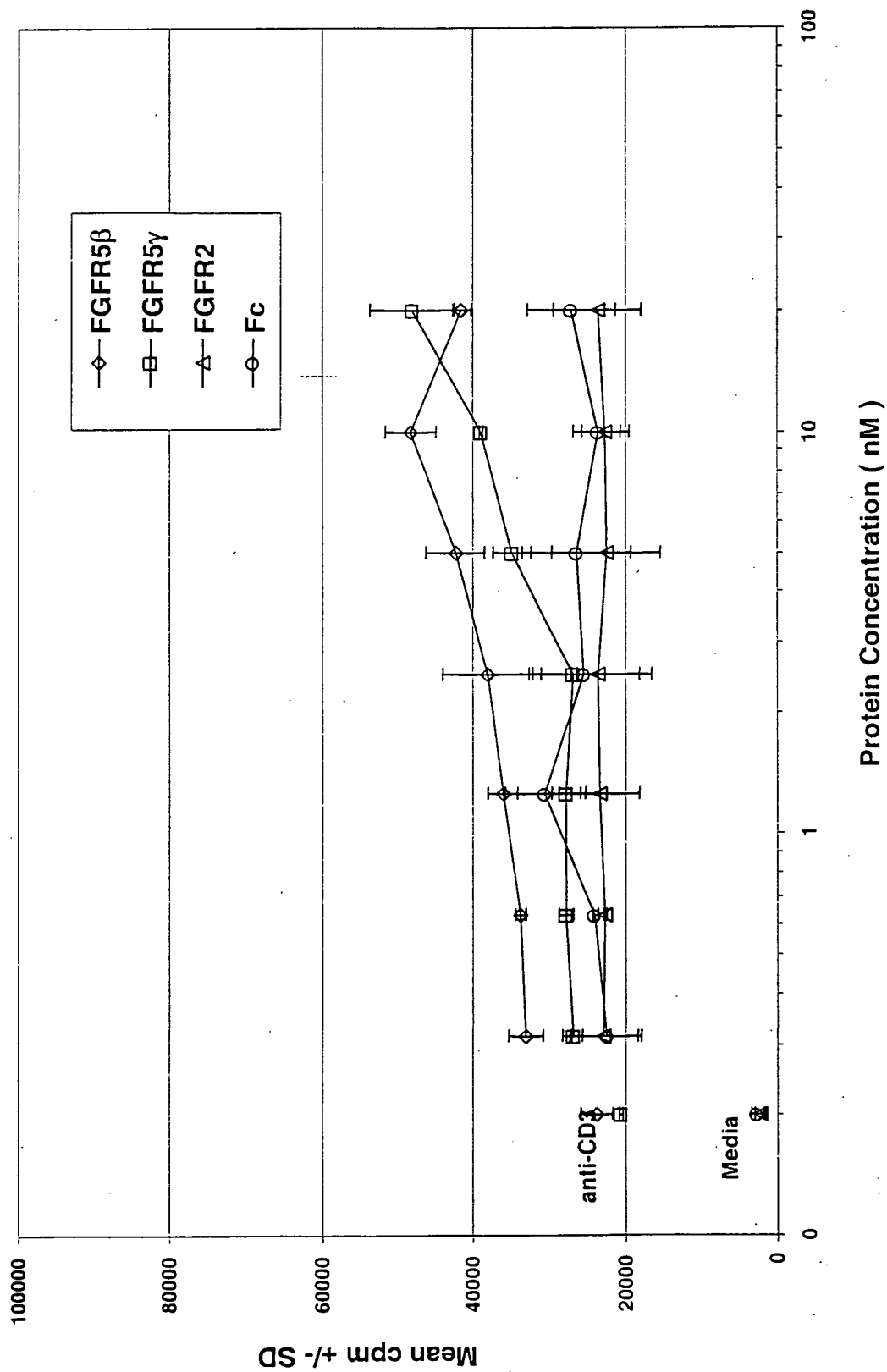


Fig. 6

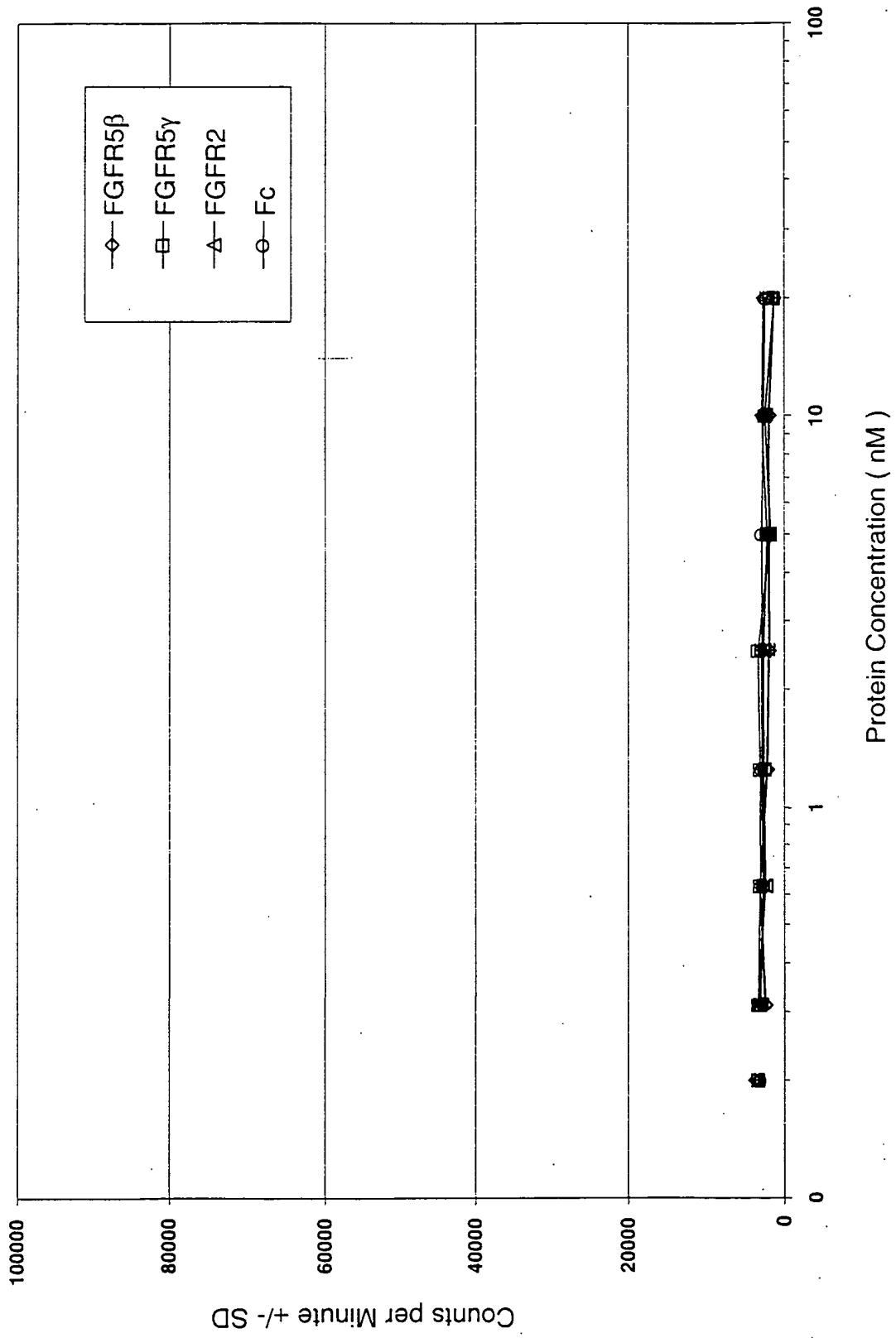


Fig. 7

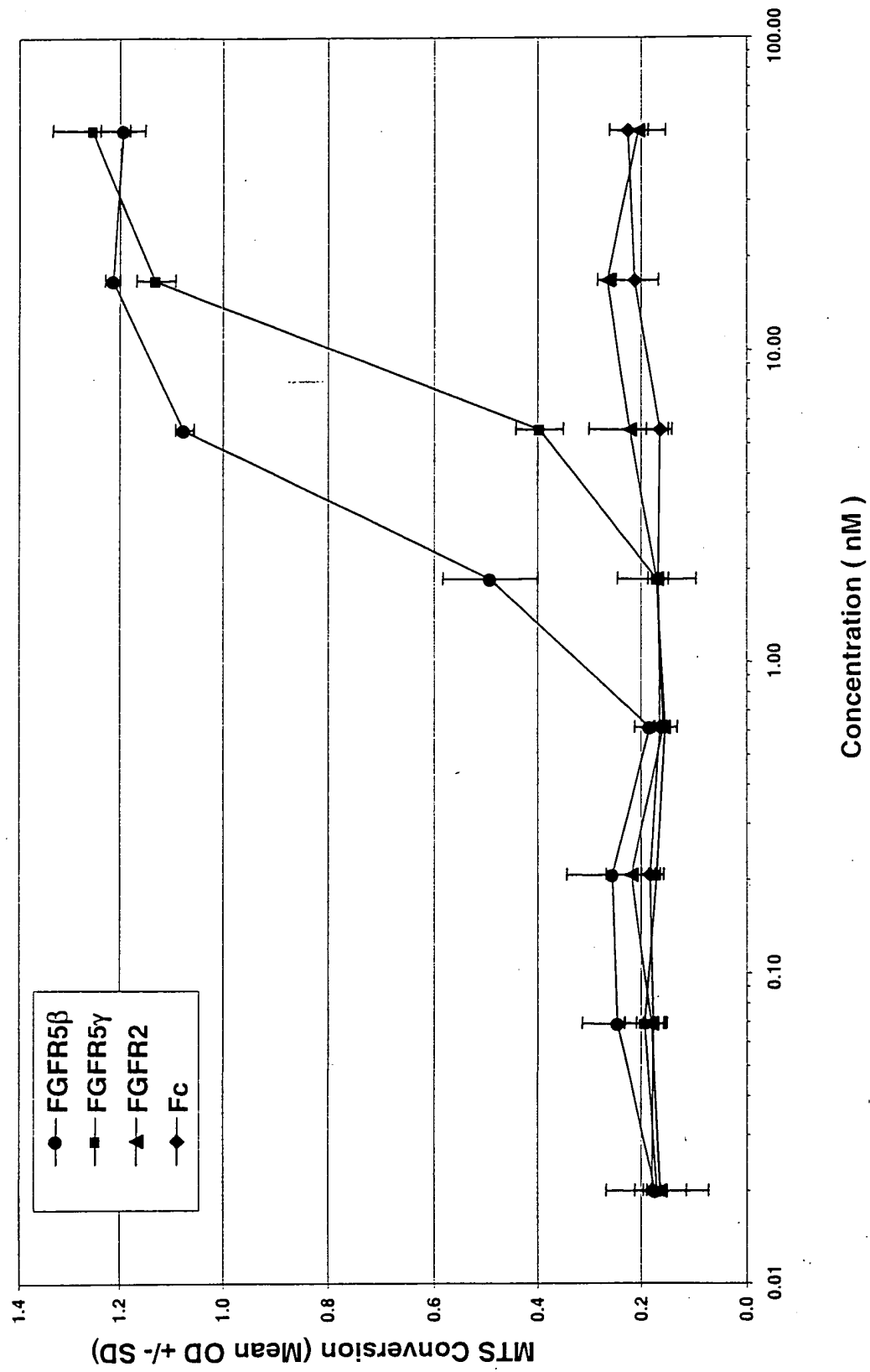


Fig. 8

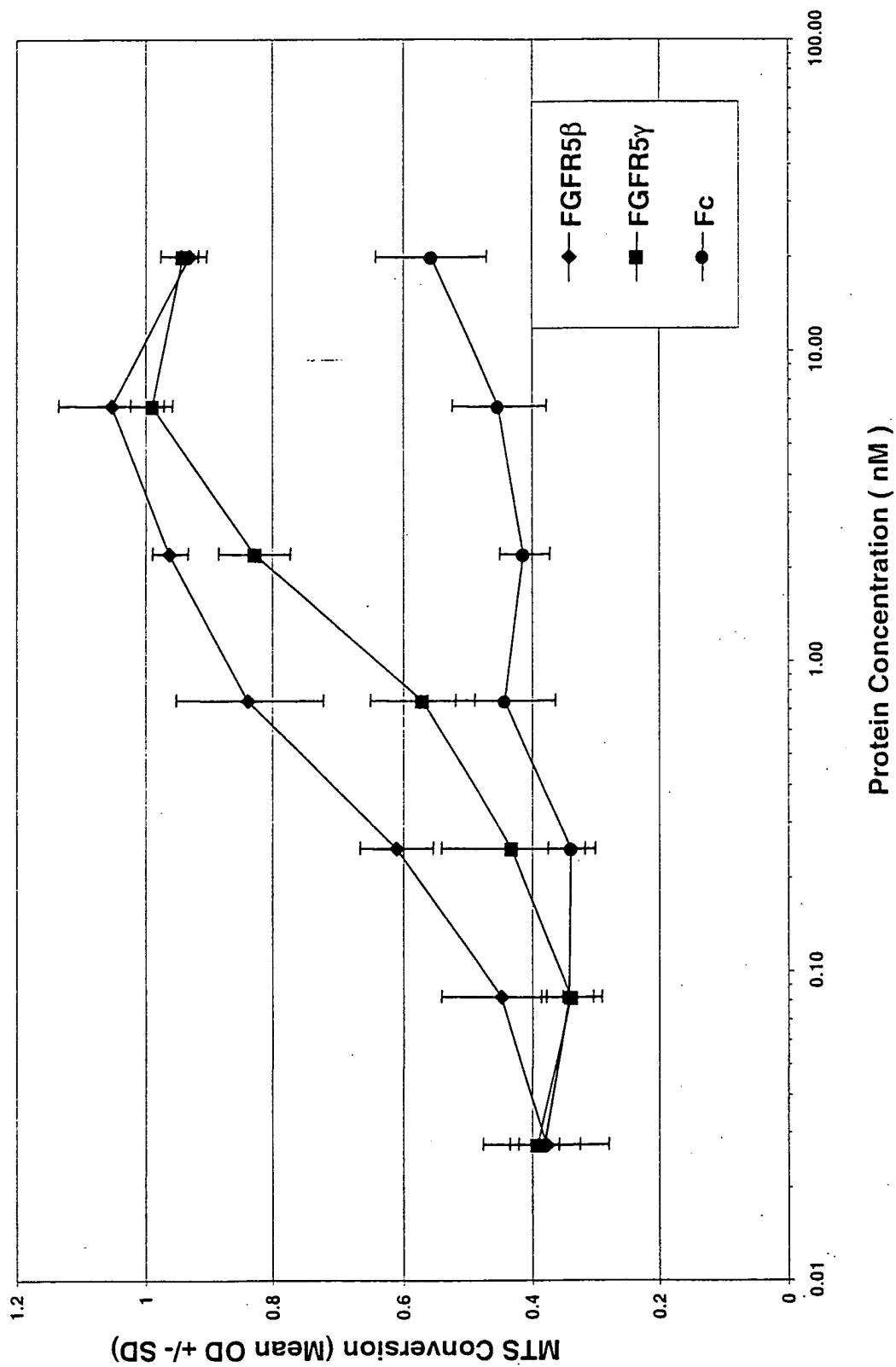
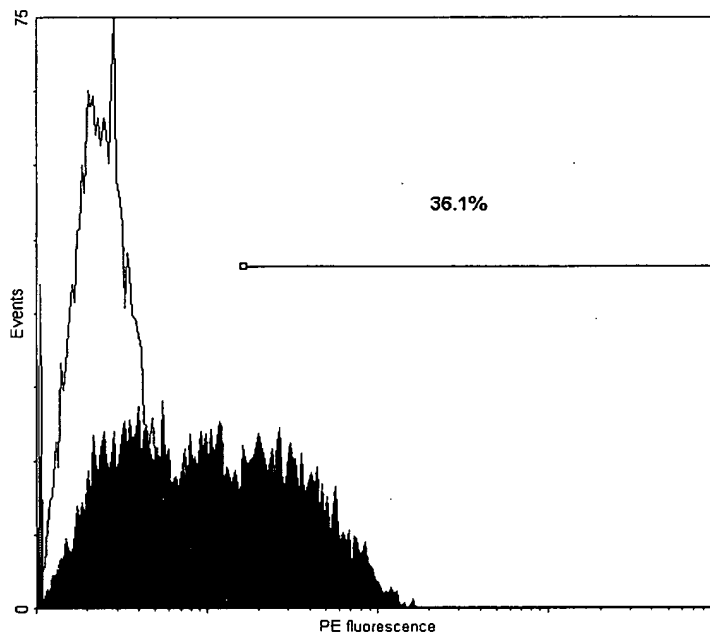


Fig. 9

FGFR5 β -treated PBMC

Overlay Plot 1



FGFR5 γ -treated PBMC

Overlay Plot 2

